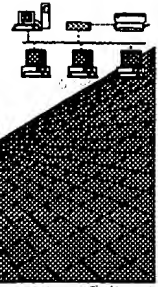


BEST AVAILABLE COPY

Batch

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/250,056

Art Unit / Team No: 1642

Date Processed by STIC: 6/22/89

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/250,056

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056DATE: 06/22/1999
TIME: 16:42:03

Input Set: I250056.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

PP-315

1 <110> APPLICANT: Marks, James D
2 Poul, Marie A
3 <120> TITLE OF INVENTION: INTERNALIZING ERBB2 ANTIBODIES
4 <130> FILE REFERENCE: 2500.114US1
5 <140> CURRENT APPLICATION NUMBER: US/09/250,056
6 <141> CURRENT FILING DATE: 1999-02-12
7 <150> EARLIER APPLICATION NUMBER: 60/082,953
8 <151> EARLIER FILING DATE: 1998-03-04
9 <160> NUMBER OF SEQ ID NOS: 4
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 246
13 <212> TYPE: PRT
14 <213> ORGANISM: Artificial Sequence
15 <220> FEATURE:
16 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv F5 amino
17 acid sequence
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20 <222> LOCATION: (31)..(35)
21 <223> OTHER INFORMATION: VH-CDR1
22 <220> FEATURE:
23 <221> NAME/KEY: DOMAIN
24 <222> LOCATION: (50)..(66)
25 <223> OTHER INFORMATION: VH-CDR2
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28 <222> LOCATION: (99)..(108)
29 <223> OTHER INFORMATION: VH-CDR-3
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32 <222> LOCATION: (157)..(170)
33 <223> OTHER INFORMATION: VL-CDR1
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41 <223> OTHER INFORMATION: VL-CDR3
42 <400> SEQUENCE: 1
43 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
44 1 5 10 15

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056

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46              20              25              30
47      Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
48              35              40              45
49      Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val
50              50              55              60
51      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
52              65              70              75              80
53      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
54              85              90              95
55      Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly
56              100             105             110
57      Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
58              115             120             125
59      Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
60              130             135             140
61      Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
62      145             150             155             160
63      Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
64              165             170             175
65      Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
66              180             185             190
67      Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
68              195             200             205
69      Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
70              210             215             220
71      Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
72      225             230             235             240
73      Lys Leu Thr Val Leu Gly
74              245

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75 <210> SEQ ID NO 2

76 <211> LENGTH: 242

77 <212> TYPE: PRT

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84 <222> LOCATION: (31)..(35)

85 <223> OTHER INFORMATION: VH-CDR2

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92 <222> LOCATION: (99)..(108)

93 <223> OTHER INFORMATION: VH-CDR3

94 <220> FEATURE:

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056

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 109 Ser. Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 110 20 25 30
 111 Ala Met Gly Trp Xaa Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 112 35 40 45
 113 Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
 114 50 55 60
 115 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 116 65 70 75 80
 117 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 118 85 90 95
 119 Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
 120 100 105 110
 121 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 122 115 120 125
 123 Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
 124 130 135 140
 125 Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
 126 145 150 155 160
 127 Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 128 165 170 175
 129 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 130 180 185 190
 131 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 132 195 200 205
 133 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 134 210 215 220
 135 Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
 136 225 230 235 240
 137 Lys Arg
 138 <210> SEQ ID NO 3
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 140 <212> TYPE: DNA
 141 <213> ORGANISM: Artificial Sequence
 142 <220> FEATURE:
 143 <223> OTHER INFORMATION: Description of Artificial Sequence: scF5 single
 144 chain Ab

W-->

see
 item 10
 in even
 summary
 sheet

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056

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Input Set: I250056.RAW

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155 <222> LOCATION: (295)..(324)
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168 <223> OTHER INFORMATION: VL-CDR3
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172      ccagggaagg ggctggagtg ggtctcagct attagtggtc gtggtgataa cacatactac 180
173      gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
174      ctgcaaataa acagcctgag agccgaggac acggccggtt attactgtgc gaaaatgaca 300
175      agtaacgcgt tcgcatttga ctactggggc caggggaaccc tggtcaccgt ctcctcagggt 360
176      ggaggcgggt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
177      ccgccctcag tgtctggggc cccagggcag agggtcacca tctcctgcac tgggagcagc 480
178      tccaacatcg gggcagggtta tgggtgtacac tggtagcagc agcttccagg aacagccccc 540
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180      ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct 660
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189      chain Ab
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192 <222> LOCATION: (91)..(105)
193 <223> OTHER INFORMATION: VH-CDR1
194 <220> FEATURE:

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197 <223> OTHER INFORMATION: VH-CDR2
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217 ccagggaagg ggctggagtg ggtctcatca attagtggca gtagtagata catatattac 180
218 gcagactccg tgaagggccg gttcaccatc tcccgagaca attccaagaa cacgctgtat 240
219 ctgcaaatac acagcctgcg agccgaggac acggccgttt attactgtgc gaaaatggat 300
220 gcttcgggga gttatttttaa tttctggggc cagggcaccc tggtcaccgt ctctcagggt 360
221 ggaggcgggt caggcggagg tggctctggc ggtggcggat cggaaaacgac actcacgcag 420
222 tctccatcct tcctgtctgc attttagtaga gacagaatca ccatcacttg ccgggccagt 480
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224 ctgatctatg ctgcatccac tttgcaaagt ggggtcccat caaggttcag cggcagtgga 600
225 tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
226 tattgtcaac aatataatag ttaccctctc agtttcggcg gagggaccaa ggtggagatc 720
227 aaacgt 726

*all from 10 on Enr
summary
sheet*

Input Set: I250056.RAW

Line	Error/Warning	Original Text
111	W "N" or "Xaa" used: Feature required	Ala Met Gly Trp Xaa Arg Gln Ala Pro Gly L
216	W "N" or "Xaa" used: Feature required	tcctgtgcag cctctggatt cacctttagc agctatgc

Application No. 09/250,056

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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